Received: 8 January 2026 | Accepted: 3 April 2026

DOI: 10.1111/afe.70053

SHORT COMMUNICATION

Agricultural and Forest Entomology

Development and survival of *Bemisia tabaci* MEAM1 (Hemiptera: Aleyrodidae) on *Eucalyptus* genotypes

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Funding information
Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Grant/Award Number: 88887.160665/2025-00; Conselho Nacional de Desenvolvimento Científico e Tecnológico

Abstract

1. *Bemisia tabaci* MEAM1 is a highly polyphagous pest widely distributed in Brazil, causing direct and indirect damage in agricultural systems. Recent records of the presence of the *B. tabaci* in nurseries and young eucalyptus stands raise concerns about its potential establishment in forest systems, especially in agroforestry landscapes.
2. In this study, the development time and viability of *B. tabaci* MEAM1 were evaluated on two *Eucalyptus* genotypes (*Eucalyptus camaldulensis* and *Eucalyptus urophylla* × *Eucalyptus grandis*), using soybean (*Glycine max*) as a control host, under controlled laboratory conditions. Development time was analyzed using survival curves, and stage-specific viability was estimated using generalized linear models.
3. Soybean induced the shortest development times across all stages, followed by *E. camaldulensis*, while the *E. urophylla* × *E. grandis* hybrid resulted in the longest development times. Viability followed the same pattern, with the highest on soybean, intermediate on *E. camaldulensis* and the lowest on the hybrid.
4. Despite the observed differences, both evaluated *Eucalyptus* genotypes allowed complete development of *B. tabaci* MEAM1 under controlled laboratory conditions, providing preliminary evidence of host suitability.

KEYWORDS
polyphagy, whitefly host plants, whitefly life history

INTRODUCTION

The genus *Eucalyptus* L'Hér., native to Australia and introduced to Brazil, has become a major component of the Brazilian planted tree sector over recent decades. In recent reports, the total area of planted trees in Brazil has exceeded 10 million ha, with approximately 77% comprising *Eucalyptus* species (Ibá, 2025). In recent decades, the expansion of agricultural areas and forest plantations has profoundly altered the Brazilian landscape, increasing connectivity between these production systems and creating new interfaces between agricultural and forest environments (Ratke et al., 2024). This landscape configuration facilitates the dispersal and colonization of polyphagous pests from agricultural crops into forestry areas, elevating the risk of novel insect–plant interactions in forest systems (Borges Junior et al., 2020).

Among the polyphagous insects capable of exploiting these diverse environments, the whitefly *Bemisia tabaci* (Gennadius, 1889) (Hemiptera: Aleyrodidae) is particularly prominent. It is recognized as a complex of cryptic species (MacLeod et al., 2022), within which

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B. tabaci MEAM1 (Middle East–Asia Minor 1) is one of the most widely distributed and invasive (Peng et al., 2025). Damage caused by *B. tabaci* MEAM1 can be direct, through phloem feeding, or indirect, via honeydew excretion and transmission of plant viruses, leading to substantial yield losses in numerous crops (Lourenção et al., 2015; Polston et al., 2014).

The high polyphagy of *B. tabaci* MEAM1 enables the insect to develop and reproduce on a wide range of plant species, including ornamental, agricultural and weed hosts, as well as certain forest species (Ferreira et al., 2008; Sacilotto et al., 2024; Shi et al., 2023). In agroforestry landscapes, this polyphagous capacity promotes seasonal migration among hosts, allowing population persistence on alternative plants during crop off-seasons and facilitating subsequent recolonization of preferred agricultural crops (Togni et al., 2021).

Although there are increasing records of the *B. tabaci* complex in eucalyptus nurseries and young stands (A. C. V. Lima, personal communication, 2024), studies remain scarce, and to date, there are no formal reports of economic damage or direct losses caused by this pest on this host. Available references on the *B. tabaci* complex are predominantly descriptive and generally limited to documenting its occurrence in production nurseries, without providing additional information on biological performance (de Queiroz et al., 2021; Santos et al., 2008). Among these records, the study by Ferreira et al. (2008) is notable for going beyond mere reporting: the authors observed that *B. tabaci* MEAM1 completed its life cycle from egg to adult on *Eucalyptus camaldulensis* Dehnh. (Myrtales: Myrtaceae) seedlings maintained in a greenhouse. However, demonstrating that the species can develop on this host is only a preliminary observation, as it lacks measurements of key biological parameters, such as development time and stage-specific viability, which are essential for assessing host suitability.

Regarding *B. tabaci*, MEAM1 is the most widely distributed and predominant species within the *B. tabaci* species complex in Brazilian agroecosystems (Fernandes et al., 2024). The use of MEAM1 in this study enables a biologically realistic assessment of the adaptation and establishment potential of this invasive pest in *Eucalyptus*. Given the scarcity of experimental studies quantifying key biological parameters of *B. tabaci* MEAM1 on *Eucalyptus* genotypes, understanding its performance on this host is essential for evaluating the pest's establishment potential in forest systems and the associated risks in integrated agricultural–forestry landscapes. In this context, the objective of this study was to evaluate the development time and viability of *B. tabaci* MEAM1 on two *Eucalyptus* genotypes, with simultaneous comparisons to soybean, under controlled laboratory conditions.

MATERIALS AND METHODS

Plant selection

The plants used in the experiments were the soybean *Glycine max* (L.) Merr. (Fabales: Fabaceae) and two *Eucalyptus* genotypes: *E. camaldulensis* and the hybrid *Eucalyptus urophylla* S. T. Blake × *Eucalyptus grandis* W. Hill ex Maiden (Myrtales: Myrtaceae). Soybean was used as the control host because it is a well-documented preferred host of *B. tabaci* MEAM1 in Brazil (do Valle et al., 2012). Plants were grown in 420-mL pots containing a commercial substrate composed of pine bark, peat and expanded vermiculite (Vida Verde®, Grupo Provaso, Brazil) and irrigated daily. Plant age was standardized at 20 days for soybean and 3 months for *Eucalyptus* genotypes. All plants were maintained under pesticide-free conditions.

Establishment and maintenance of the *B. tabaci* MEAM1 colony

The insects used in the experiments were obtained from a previously established greenhouse colony maintained on cabbage, *Brassica oleracea* L. var. *acephala* DC. (Brassicales: Brassicaceae). The identity of *B. tabaci* MEAM1 was confirmed using the molecular markers and methods described by De Barro et al. (2003).

Egg-to-adult development of *B. tabaci* MEAM1

The experiment was conducted in climate-controlled chambers set at 26 ± 2°C and 70% ± 10% relative humidity (RH) (chamber set-point variation), with a 14-h photoperiod. For each plant, a single fully expanded apical leaf was selected and isolated. To infest leaves, 50 pairs of adult whiteflies were collected from the stock colony using an entomological aspirator and confined within organza bag cages (7 × 9 cm) tied to the petiole of the selected leaf with satin ribbon. Adults were allowed to oviposit for 4 h, a period sufficient to ensure adequate egg laying and uniformity in egg age.

After the oviposition period, cages were removed, and adult insects were aspirated from the plants. The abaxial surface of each leaf was then examined under a stereomicroscope (40× magnification), and 12 eggs per leaf were selected and marked with a non-toxic felt-tip marker (Posca PC-1M). Plants were subsequently transferred to climate-controlled chambers, where insect development and survival were monitored. Evaluations were conducted daily at 10:00 h to record the following parameters: duration and viability of the egg stage, duration and viability of the nymphal stage, total egg-to-adult development time and overall viability (egg-to-adult survival).

The experiment followed a completely randomized design with 3 treatments (hosts) and 10 independent plants per treatment ($n = 10$). Each plant consisted of one infested leaf containing 12 individually marked eggs monitored throughout development, totalling 120 individuals per treatment. One replicate of the *E. urophylla* × *E. grandis* treatment was lost during the experiment and excluded from the analyses.

Statistical analysis

Data on developmental stage duration of *B. tabaci* MEAM1 were analysed using Kaplan–Meier survival analysis (Kaplan & Meier, 1958),

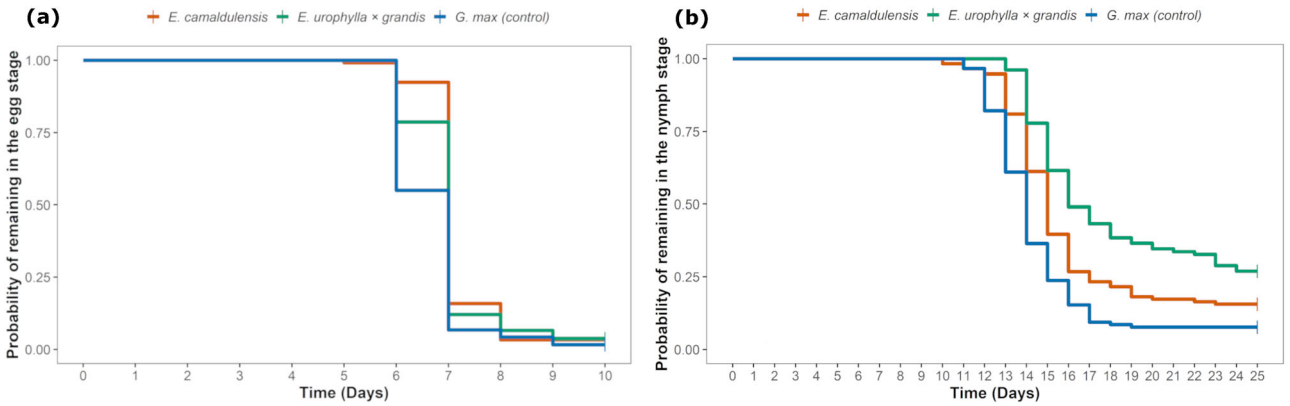


FIGURE 1 Kaplan–Meier survival curves of *Bemisia tabaci* MEAM1 on soybean (*Glycine max*; control), *Eucalyptus camaldulensis* and the *Eucalyptus urophylla* × *Eucalyptus grandis* hybrid under experimental conditions. (a) Probability of individuals remaining in the egg stage (i.e., not hatching). (b) Probability of individuals remaining in the nymphal stage (i.e., not emerging as adults).

with incomplete observations included when stage transitions were not observed within the evaluation period. Mean developmental times were estimated for each treatment. Differences among treatments were tested using the log-rank test, followed by pairwise comparisons with the Benjamini–Hochberg correction when significant (Kleinbaum & Klein, 2012).

Egg, nymphal and egg-to-adult viability were analysed using generalized linear models (GLMs) with a binomial distribution (logit link), using soybean as the reference treatment. When significant effects were detected, treatment means were compared using Tukey-adjusted pairwise contrasts derived from the fitted model. All analyses were conducted in R version 4.4.1 (R Core Team,).

RESULTS

Development time of *B. tabaci* MEAM1

Kaplan–Meier survival curves revealed significant differences in development times of *B. tabaci* MEAM1 among host plants for the egg, nymphal and total egg-to-adult stages ($p < 0.0001$; Figures 1 and 2). Individuals reared on soybeans exhibited the fastest development across all stages, followed by *E. camaldulensis*, whereas the *E. urophylla* × *E. grandis* hybrid consistently showed the slowest development. Specifically, individuals on the hybrid had a higher probability of remaining in the egg, nymphal and total egg-to-adult stages throughout the observation period, reflecting prolonged development times compared with the other treatments.

The log-rank test confirmed significant differences in development times among treatments for the egg stage ($\chi^2 = 30.2$, df = 2, $p < 0.0001$), nymphal stage ($\chi^2 = 45.7$, df = 2, $p < 0.0001$) and total egg-to-adult period ($\chi^2 = 49.2$, df = 2, $p < 0.0001$). Pairwise comparisons, adjusted using the Benjamini–Hochberg method, revealed significant differences between soybean and both *Eucalyptus* genotypes across all stages, as well as between the two *Eucalyptus* genotypes for the nymphal stage and the total egg-to-adult period (Table 1).

The egg stage was significantly shorter on soybean than on both *Eucalyptus* genotypes, which did not differ significantly from each other. The nymphal stage was significantly longer on the *E. urophylla* × *E. grandis* hybrid than on the other hosts, resulting in the longest egg-to-adult development time for this genotype. The egg-to-adult period averaged approximately 21 days on soybean, compared with more than 23 days on the *Eucalyptus* genotypes, with the highest values recorded on the *E. urophylla* × *E. grandis* hybrid (Table 1).

Viability of life stages in *B. tabaci* MEAM1

Egg viability exceeded 96% across all hosts, with no significant differences among treatments ($\chi^2 = 1.07$, df = 2, $p = 0.587$) (Table 1). In contrast, nymphal viability was significantly affected by host treatment ($\chi^2 = 16.10$, df = 2, $p < 0.001$). Nymphs reared on soybean exhibited the highest viability, whereas those on the *Eucalyptus* genotypes showed reduced viability, particularly on the *E. urophylla* × *E. grandis* hybrid. *E. camaldulensis* displayed intermediate values, not differing significantly from soybean, while the hybrid reduced nymphal viability of *B. tabaci* MEAM1 by approximately 20% relative to soybean (Table 1).

Total egg-to-adult viability was significantly influenced by host treatment ($\chi^2 = 16.60$, df = 2, $p < 0.001$). *B. tabaci* MEAM1 exhibited the highest viability on soybean, followed by *E. camaldulensis*, with the lowest on the *E. urophylla* × *E. grandis* hybrid. Relative to soybean, the hybrid reduced overall viability by approximately 22%, whereas *E. camaldulensis* showed intermediate performance and did not differ significantly from soybean. The two *Eucalyptus* genotypes did not differ significantly (Table 1).

DISCUSSION

In the present study, we observed variations in both development time and viability of *B. tabaci* MEAM1 among the treatments

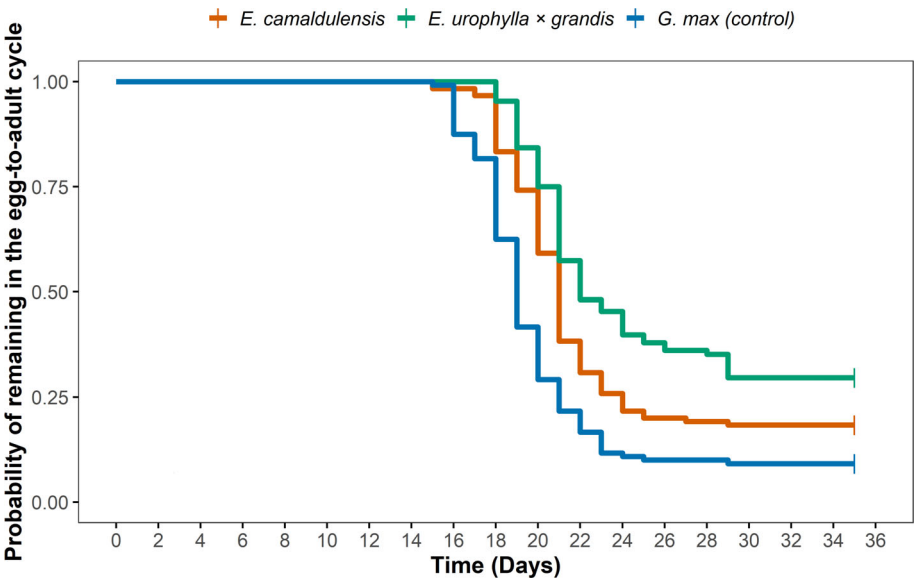


FIGURE 2 Kaplan–Meier survival curves showing the probability of *Bemisia tabaci* MEAM1 remaining in the egg-to-adult developmental cycle (i.e., not emerging as adults) on soybean (*Glycine max*; control), *Eucalyptus camaldulensis* and the *Eucalyptus urophylla* × *Eucalyptus grandis* hybrid under experimental conditions.

TABLE 1 Mean (±SE) development time (days) and viability (%) of *Bemisia tabaci* MEAM1 at the egg, nymphal and egg-adult stages on soybean (*Glycine max*, control), *Eucalyptus camaldulensis* and *Eucalyptus urophylla* × *Eucalyptus grandis* under experimental conditions.

Treatment	Egg	Nymph	Egg-adult
Development time (days)			
G. max	6.67 ± 0.07a ($n = 120$)	14.78 ± 0.30a ($n = 118$)	20.57 ± 0.46a ($n = 120$)
E. camaldulensis	7.14 ± 0.06b ($n = 120$)	16.43 ± 0.39b ($n = 116$)	23.15 ± 0.55b ($n = 120$)
E. urophylla × *E. grandis*	7.00 ± 0.08b ($n = 108$)	18.59 ± 0.45c ($n = 104$)	25.68 ± 0.63c ($n = 108$)
Viability (%)			
G. max	98.33 ± 1.17a ($n = 10$)	93.22 ± 2.31a ($n = 10$)	91.67 ± 2.52a ($n = 10$)
E. camaldulensis	96.67 ± 1.64a ($n = 10$)	86.21 ± 3.20ab ($n = 10$)	83.33 ± 3.40ab ($n = 10$)
E. urophylla × *E. grandis*	96.30 ± 1.82a ($n = 9$)	74.04 ± 4.30b ($n = 9$)	71.30 ± 4.35b ($n = 9$)

Note: Development times were estimated from Kaplan–Meier survival analysis (n = number of individuals per stage). Viability was analysed using a binomial generalized linear model (GLM) based on independent plants ($n = 10$ per treatment, except *E. urophylla* × *E. grandis*, $n = 9$). Different letters indicate significant differences among treatments ($p < 0.05$).

evaluated (Table 1). Similar results, showing variations in the performance of *B. tabaci* MEAM1 on different hosts, have also been reported in studies conducted in greenhouses and laboratories, including on legume, vegetable and weed species (Sacilotto et al., 2024; Villas Bôas et al., 2002), confirming that host suitability can directly influence the insect's biological parameters.

Differences in egg incubation period among hosts were statistically significant but small (<1 day) and did not affect egg viability, which remained consistently high across treatments. Egg development in *B. tabaci* MEAM1 is influenced by egg–leaf interactions mediated by the pedicel inserted into the leaf epidermis (Buckner et al., 2002; Walker et al., 2010), and minor differences in leaf structural or chemical traits (Shah & Liu, 2013) may explain the small delays observed among hosts. Overall, the egg stage was only minimally affected by the host plant.

The differences among hosts became more pronounced during the nymphal stage. In this stage, continuous interaction with the plant phloem through feeding (Chu et al., 2007; Walker et al., 2010) can expose the insect to secondary metabolites produced by the plant, which are often associated with defence responses. Studies have shown that *B. tabaci* MEAM1 can be negatively affected by host chemical composition, with high levels of secondary metabolites leading to reduced performance during nymphal development (Guo et al., 2013). Although we did not quantify or chemically characterize the compounds present in the host species' leaves, species of the genus *Eucalyptus* generally exhibit a complex chemical composition, including various classes of secondary metabolites, particularly essential oils and phenolic compounds (Avila et al., 2022; Ohmart & Edwards, 1991). These chemical compounds vary among *Eucalyptus* species, hybrids and genotypes (Lucia et al., 2016) and can influence both the nutritional quality of the host and the

performance of phytophagous insects. This interpretation is consistent with the observed experimental patterns, in which prolonged nymphal development on the *Eucalyptus* genotypes was accompanied by reduced viability. Whereas soybean exhibited high viability (93.22%) and *E. camaldulensis* showed similar values (86.21%), the hybrid *E. urophylla* × *E. grandis* displayed a reduction of approximately 20% in nymphal viability compared to soybean, characterizing it as the least suitable host.

By integrating effects across developmental stages, the total period from egg to adult indicates that soybean is the most favourable host for *B. tabaci* MEAM1, promoting faster development and higher viability. Among the *Eucalyptus* genotypes, *E. camaldulensis* exhibited intermediate suitability, whereas the hybrid *E. urophylla* × *E. grandis* displayed lower suitability, prolonging the life cycle and significantly reducing viability. Similar results regarding differential suitability of *Eucalyptus* genotypes to sucking insects have been reported for the psyllid *Glycaspis brimblecombei* Moore (Hemiptera: Aphalaridae) in which *E. camaldulensis* showed greater susceptibility, while hybrids of *E. urophylla* × *E. grandis* exhibited higher resistance (Pereira et al., 2020). These findings reinforce the idea that the evaluated *Eucalyptus* genotypes may differ in their susceptibility to phloem-feeding insects, as demonstrated here for *B. tabaci* MEAM1 and previously reported for *G. brimblecombei*.

Despite the reduced performance compared with soybean, both evaluated genotypes allowed completion of the life cycle of *B. tabaci* MEAM1 under controlled laboratory conditions, indicating potential host suitability in this experimental context. However, extrapolation to field conditions should be made with caution, as reproductive performance, plant age, environmental variability and natural enemies may influence population establishment. Because only two genotypes were evaluated and reproductive parameters were not assessed, conclusions regarding the role of *Eucalyptus* as an alternative host remain preliminary. Future field studies integrating fecundity and ecological variables such as plant age, seasonality, microclimatic variation, host composition and natural enemies will be necessary to clarify better the role of *Eucalyptus* in whitefly population dynamics in agroforestry systems.

AUTHOR CONTRIBUTIONS

Luis Gustavo Talarico Rubim: Conceptualization; methodology; data curation; formal analysis; writing — original draft. **Anna Mara Ferreira Maciel:** Methodology; data curation; writing — review and editing. **André Luiz Lourenção:** Supervision; writing — review and editing. **Alexandre Coutinho Vianna Lima:** Writing — review and editing. **Wesley Augusto Conde Godoy:** Conceptualization; supervision; writing — review and editing.

ACKNOWLEDGEMENTS

The Brazilian Federal Agency for Support and Evaluation of Graduate Education (CAPES, grant no. 88887.160665/2025-00) provided financial support through a scholarship to LGTL. ALL and WACG received productivity research grants from the National Council for Scientific and Technological Development (CNPq). The Article Processing Charge for the publication of this research was funded by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) (ROR identifier: 00x0ma614).

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in Zenodo at https://doi.org/10.5281/zenodo.18865040 (Rubim, 2026).

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How to cite this article: Rubim, L.G.T., Ferreira Maciel, A.M., Lourenção, A.L., Lima, A.C.V. & Godoy, W.A.C. (2026) Development and survival of *Bemisia tabaci* MEAM1 (Hemiptera: Aleyrodidae) on *Eucalyptus* genotypes. *Agricultural and Forest Entomology*, 28(4), 671–676. Available from: https://doi.org/10.1111/afe.70053